Figure 1

```
1    GAGAAGAGAGTTTTGTAGCGAGCTCGCGCGAATGCGAAGCCAACCGAGAGAGGTCTCGATACCAAATCCCGATTTCTCAACCTGAATCCCCCCCCCACGT
101  TCCTCGTTTCAATCTGTTCGTCTGCGAATCGAATTCTTTGTTTTTTTTTCTCTAATTTTACCGGGAATTGTCGAATTAGGCATTCACCAACGAGCAAGAG
201  GGGAGTGGATTGGTTGGTTAAAGCTCCGCATCTTGCGGCGGAAATCTCGCTCTCTTCTCTGCGGTGGGTGGCCGGAGAAGTCGCCGCCGGTGAGGCATGG
                                                                                                      M  G

301  GGATGGAGGTGGCGGCGGCGCGGCTGGGGGCTCTGTACACGACCTCCGACTACGCGTCGGTGGTGTCCATCAACCTGTTCGTCGCGCTGCTCTGCGCCTG
       M  E  V  A  A  A  R  L  G  A  L  Y  T  T  S  D  Y  A  S  V  V  S  I  N  L  F  V  A  L  L  C  A  C

401  CATCGTCCTCGGCCACCTCCTCGAGGAGAATCGCTGGGTCAATGAGTCCATCACCGCGCTCATCATCGGGCTCTGCACCGGCGTGGTGATCTTGCTGATG
      I  V  L  G  H  L  L  E  E  N  R  W  V  N  E  S  I  T  A  L  I  I  G  L  C  T  G  V  V  I  L  L  M

501  ACCAAAGGGAAGAGCTCGCACTTATTCGTCTTCAGTGAGGATCTCTTCTTCATCTACCTCCTCCCTCCGATCATCTTCAATGCAGGTTTTCAGGTAAAGA
     T  K  G  K  S  S  H  L  F  V  F  S  E  D  L  F  F  I  Y  L  L  P  P  I  I  F  N  A  G  F  Q  V  K  K

601  AAAAGCAATTCTTCCGGAATTTCATGACGATCACATTATTTGGAGCCGTCGGGACAATGATATCCTTTTTCACAATATCTATTGCTGCCATTGCAATATT
       K  Q  F  F  R  N  F  M  T  I  T  L  F  G  A  V  G  T  M  I  S  F  F  T  I  S  I  A  A  I  A  I  F

701  CAGCAGAATGAACATTGGAACGCTGGATGTAGGAGATTTTCTTGCAATTGGAGCCATCTTTTCTGCGACAGATTCTGTCTGCACATTGCAGGTCCTCAAT
       S  R  M  N  I  G  T  L  D  V  G  D  F  L  A  I  G  A  I  F  S  A  T  D  S  V  C  T  L  Q  V  L  N

801  CAGGATGAGACACCCTTTTTGTACAGTCTGGTATTCGGTGAAGGTGTTGTGAACGATGCTACATCAATTGTGCTTTTCAACGCACTACAGAACTTTGATC
     Q  D  E  T  P  F  L  Y  S  L  V  F  G  E  G  V  V  N  D  A  T  S  I  V  L  F  N  A  L  Q  N  F  D  L

901  TTGTCCACATAGATGCGGCTGTCGTTCTGAAATTCTTGGGGAACTTCTTTTATTTATTTTTGTCGAGCACCTTCCTTGGAGTATTTGCTGGATTGCTCAG
       V  H  I  D  A  A  V  V  L  K  F  L  G  N  F  F  Y  L  F  L  S  S  T  F  L  G  V  F  A  G  L  L  S

1001 TGCATACATAATCAAGAAGCTATACATTGGAAGGCATTCTACTGACCGTGAGGTTGCCCTTATGATGCTCATGGCTTACCTTTCATATATGCTGGCTGAG
       A  Y  I  I  K  K  L  Y  I  G  R  H  S  T  D  R  E  V  A  L  M  M  L  M  A  Y  L  S  Y  M  L  A  E

1101 TTGCTAGATTTGAGCGGCATTCTCACCGTATTCTTCTGTGGTATTGTAATGTCACATTACACTTGGCATAACGTCACAGAGAGTTCAAGAGTTACAACAA
     L  L  D  L  S  G  I  L  T  V  F  F  C  G  I  V  M  S  H  Y  T  W  H  N  V  T  E  S  S  R  V  T  T  K

1201 AGCACGCATTTGCAACTCTGTCCTTCATTGCTGAGACTTTTCTCTTCCTGTATGTTGGGATGGATGCATTGGATATTGAAAAATGGGAGTTTGCCAGTGA
       H  A  F  A  T  L  S  F  I  A  E  T  F  L  F  L  Y  V  G  M  D  A  L  D  I  E  K  W  E  F  A  S  D

1301 CAGACCTGGCAAATCCATTGGCATAAGCTCAATTTTGCTAGGATTGGTTCTGATTGGAAGAGCTGCTTTTGTATTCCCGCTCTCGTTCTTGTCGAACCTA
       R  P  G  K  S  I  G  I  S  S  I  L  L  G  L  V  L  I  G  R  A  A  F  V  F  P  L  S  F  L  S  N  L

1401 ACAAAGAAGGCACCGAATGAAAAAATAACCTGGAGACAGCAAGTTGTAATATGGTGGGCTGGGCTGATGAGAGGAGCTGTGTCGATTGCTCTTGCTTACA
     T  K  K  A  P  N  E  K  I  T  W  R  Q  Q  V  V  I  W  W  A  G  L  M  R  G  A  V  S  I  A  L  A  Y  N

1501 ATAAGTTTACAAGATCTGGCCATACTCAGCTGCACGGCAATGCAATAATGATCACCAGCACCATCACTGTCGTTCTTTTTAGCACTATGGTATTTGGGAT
       K  F  T  R  S  G  H  T  Q  L  H  G  N  A  I  M  I  T  S  T  I  T  V  V  L  F  S  T  M  V  F  G  M

1601 GATGACAAAGCCATTGATCAGGCTGCTGCTACCGGCCTCAGGCCATCCTGTCACCTCTGAGCCTTCATCACCAAAGTCCCTGCATTCTCCTCTCCTGACA
       M  T  K  P  L  I  R  L  L  L  P  A  S  G  H  P  V  T  S  E  P  S  S  P  K  S  L  H  S  P  L  L  T

1701 AGCATGCAAGGTTCTGACCTCGAGAGTACAACCAACATTGTGAGGCCTTCCAGCCTCCGGATGCTCCTCACCAAGCCGACCCACACTGTCCACTACTACT
     S  M  Q  G  S  D  L  E  S  T  T  N  I  V  R  P  S  S  L  R  M  L  L  T  K  P  T  H  T  V  H  Y  Y  W

1801 GGCGCAAGTTCGACGACGCGCTCATGCGACCGATGTTTGGCGGGCGCGGGTTCGTGCCCTTCTCCCCTGGATCACCAACCGAGCAGAGCCATGGAGGAAG
       R  K  F  D  D  A  L  M  R  P  M  F  G  G  R  G  F  V  P  F  S  P  G  S  P  T  E  Q  S  H  G  G  R

1901 ATGAACAGTGCAAAGAAATGAGAATGGAATGGTTGATGAGGAGAATACATGTAAAATGTGACAGCAAAAGAGACAAGGCAACTTTTGGGTTTGTAGAGTT
2001 TGGCTGCTGCTAATGAGTTGTTGATAGTGCCTATATTCTTCAGAACTTCAGATGGTGCCTCACCAAGGCCTAAGAGCCAGGAGGACCTTCTGATAATGGT
2101 TCGGGATGATTGGTTTGTTCTGTCAGGATGAACCCTAGTGAGTGACACAGGGTGATGTGCTCCGACAACCTGTAAATTTTGTAGATTAACAGCCCCATTT
2201 GTACCTGTCTACCATCTTTAGTTGGCGGGTGTTCTTTCCTAGTTGCCACCCTGCATGTAAAATGAAATTCTCCGCCAAAATAGATTTGTGTGTATAATAA
2301 TTTTGCTTGCTTGAAAAAAAAAAAAAAAAA
```

Figure 2

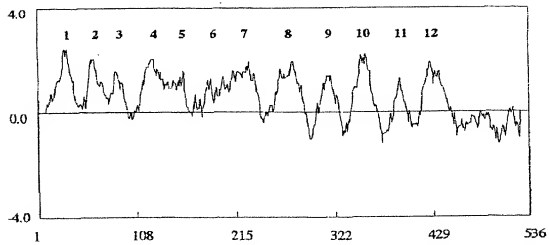


Figure 3

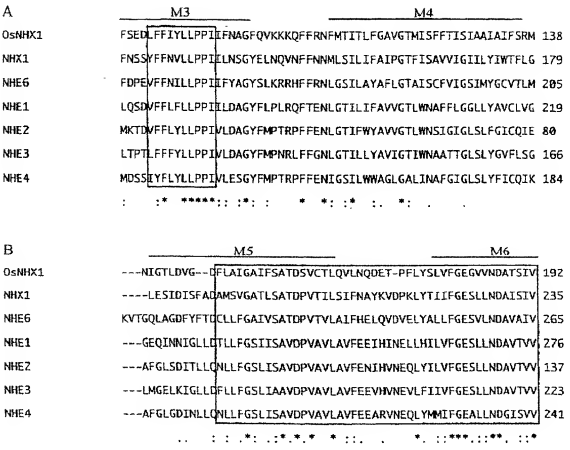

A
M3
M4
OsNHX1 FSEDLFFIYLLPPIIFNAGFQVKKKQFFRNFMTITLFGAVGTMISFFTISIAAIAIFSRM 138
NHX1 FNSSYFFNVLLPPILNSGYELNQVNFFNNMLSILIFAIPGTFISAVVIGIILYIWTFLG 179
NHE6 FDPEVFFNILLPPIIFYAGYSLKRRHFFRNLGSILAYAFLGTAISCFVIGSIMYGCVTLM 205
NHE1 LQSDVFFLFLLPPIILDAGYFLPLRQFTENLGTILIFAVVGTLWNAFFLGGLLYAVCLVG 219
NHE2 MKTDVFFLYLLPPIVLDAGYFMPTRPFFENLGTIFWYAVVGTLWNSIGIGLSLFGICQIE 80
NHE3 LTPTLFFFYLLPPIVLDAGYFMPNRLFFGNLGTILLYAVIGTIWNAATTGLSLYGVFLSG 166
NHE4 MDSSIYFLYLLPPIVLESGYFMPTRPFFENIGSILWWAGLGALINAFGIGLSLYFICQIK 184
M5
M6
OsNHX1 ---NIGTLDVG--DFLAIGAIFSATDSVCTLQVLNQDET-PFLYSLVFGEGVVNDATSIV 192
NHX1 ----LESIDISFADAMSVGATLSATDPVTILSIFNAYKVDPKLYTIIFGESLLNDAISIV 235
NHE6 KVTGQLAGDFYFTQCLLFGAIVSATDPVTVLAIFHELQVDVELYALLFGESVLNDAVAIV 265
NHE1 ---GEQINNIGLLQTLLFGSIISAVDPVAVLAVFEEIHINELLHILVFGESLLNDAVTVV 276
NHE2 ---AFGLSDITLLQNLLFGSLISAVDPVAVLAVFENIHVNEQLYILVFGESLLNDAVTVV 137
NHE3 ---LMGELKIGLLQFLLFGSLIAAVDPVAVLAVFEEVHVNEVLFIIVFGESLLNDAVTVV 223
NHE4 ---AFGLGDINLLQNLLFGSLISAVDPVAVLAVFEEARVNEQLYMMIFGEALLNDGISVV 241

Figure 4

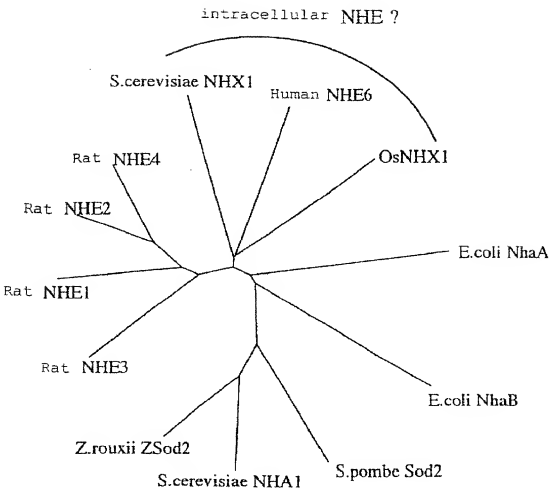

intracellular NHE ?
S.cerevisiae NHX1
Human NHE6
Rat NHE4
OsNHX1
Rat NHE2
E.coli NhaA
Rat NHE1
Rat NHE3
E.coli NhaB
Z.rouxii ZSod2
S.pombe Sod2
S.cerevisiae NHA1

Figure 5

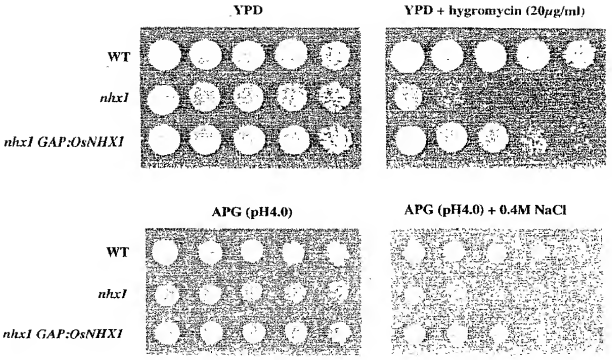
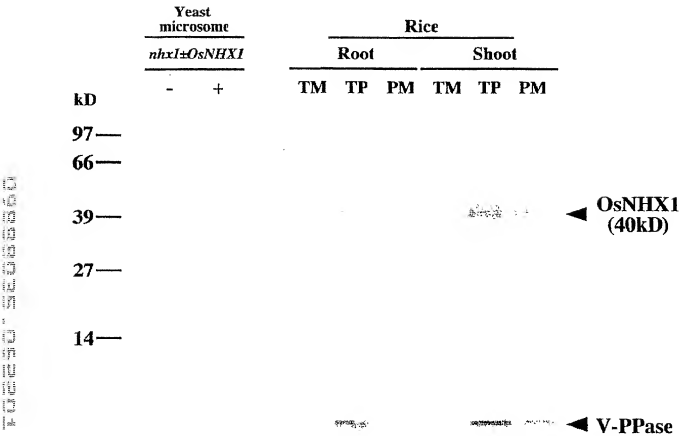

YPD
YPD + hygromycin (20μg/ml)
WT
nhx1
nhx1 GAP:OsNHX1
APG (pH4.0)
APG (pH4.0) + 0.4M NaCl
WT
nhx1
nhx1 GAP:OsNHX1

Figure 6


Yeast microsome
nhx1±OsNHX1
-
+
Rice
Root
Shoot
TM
TP
PM
TM
TP
PM
kD
97
66
39
27
14
OsNHX1 (40kD)
V-PPase